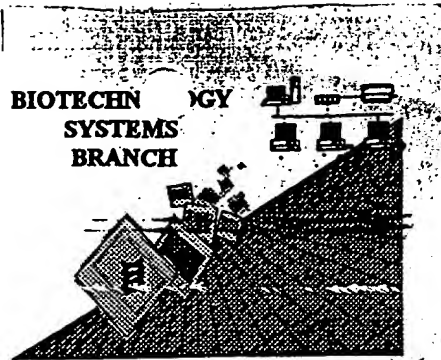


11 Dibrino

BIOTECHN  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/375,924

Source: 1644

Date Processed by STIC: 9-6-00

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY**  
or,
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/375,924

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
Indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence-Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1644

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/375,924  
DATE: 09/06/2000  
TIME: 10:47:16  
Input Set : A:\ABGX-2 CIP.txt  
Output Set: N:\CRF3\09062000\I375924.raw

4 <110> APPLICANT: Gallo, Michael  
5 Foord, Orit  
6 Junghans, Richard  
9 <120> TITLE OF INVENTION: Generation of Modified Molecules with  
10 Increased Serum Half-Lives  
13 <130> FILE REFERENCE: ABGX-2 CIP  
15 <140> CURRENT APPLICATION NUMBER: 09/375,924  
16 <141> CURRENT FILING DATE: 1999-08-17  
18 <150> PRIOR APPLICATION NUMBER: 60/096,868  
19 <151> PRIOR FILING DATE: 1998-08-17  
21 <160> NUMBER OF SEQ ID NOS: 10  
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 16  
27 <212> TYPE: PRT  
28 <213> ORGANISM: Homo sapiens  
30 <400> SEQUENCE: 1  
31 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr His Thr Cys Pro Pro  
32 1 5 10 15  
34 <210> SEQ ID NO: 2  
35 <211> LENGTH: 16  
36 <212> TYPE: PRT  
37 <213> ORGANISM: Artificial Sequence  
W--> 39 <220> FEATURE:  
W--> 39 <223> OTHER INFORMATION:  
39 <400> SEQUENCE: 2  
40 Ala Glu Pro Lys Ser Ser Asp Lys Thr His Thr His Thr Cys Pro Pro  
41 1 5 10 15  
43 <210> SEQ ID NO: 3  
44 <211> LENGTH: 12  
45 <212> TYPE: PRT  
46 <213> ORGANISM: Homo sapiens  
48 <400> SEQUENCE: 3  
49 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro  
50 1 5 10  
52 <210> SEQ ID NO: 4  
53 <211> LENGTH: 12  
54 <212> TYPE: PRT  
55 <213> ORGANISM: Homo sapiens  
57 <400> SEQUENCE: 4  
58 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro  
59 1 5 10  
61 <210> SEQ ID NO: 5  
62 <211> LENGTH: 12  
63 <212> TYPE: DNA  
64 <213> ORGANISM: Homo sapiens  
66 <400> SEQUENCE: 5

missing mandatory <220>, <223>  
features to explain source of  
genetic material  
for artificial sequence.

See #12 on Error  
Summary Sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/375,924

DATE: 09/06/2000  
TIME: 10:47:16

Input Set : A:\ABGX-2 CIP.txt  
Output Set: N:\CRF3\09062000\I375924.raw

12

67 tctctgggta aa  
69 <210> SEQ ID NO: 6  
70 <211> LENGTH: 12  
71 <212> TYPE: DNA  
72 <213> ORGANISM: Artificial Sequence

W--> 74 <220> FEATURE:  
W--> 74 <223> OTHER INFORMATION:

74 <400> SEQUENCE: 6

75 tccttaggga ag

77 <210> SEQ ID NO: 7

78 <211> LENGTH: 22

79 <212> TYPE: DNA

80 <213> ORGANISM: Artificial Sequence

W--> 82 <220> FEATURE:

W--> 82 <223> OTHER INFORMATION:

82 <400> SEQUENCE: 7

83 gggaccacg gggcgaggg gc

85 <210> SEQ ID NO: 8

86 <211> LENGTH: 36

87 <212> TYPE: DNA

88 <213> ORGANISM: Artificial Sequence

W--> 90 <220> FEATURE:

W--> 90 <223> OTHER INFORMATION:

90 <400> SEQUENCE: 8

91 cttccctaag gacatggaga ggctcttctg tgtgtg

93 <210> SEQ ID NO: 9

94 <211> LENGTH: 36

95 <212> TYPE: DNA

96 <213> ORGANISM: Artificial Sequence

W--> 98 <220> FEATURE:

W--> 98 <223> OTHER INFORMATION:

98 <400> SEQUENCE: 9

99 gattccttag ggaaggcaga gcccaaatct agtgac

101 <210> SEQ ID NO: 10

102 <211> LENGTH: 34

103 <212> TYPE: DNA

104 <213> ORGANISM: Artificial Sequence

W--> 106 <220> FEATURE:

W--> 106 <223> OTHER INFORMATION:

106 <400> SEQUENCE: 10

107 gccggaattc ggtacgtgcc aagcatcctc gtgc

36

34

Missing mandatory <220>, <223>  
features to explain source of  
genetic material for artificial  
sequence. See #12 on Error  
Summary Sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/375,924

DATE: 09/06/2000

TIME: 10:47:17

Input Set : A:\ABGX-2 CIP.txt

Output Set: N:\CRF3\09062000\I375924.raw

L:39 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:39 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:74 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:74 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:82 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:82 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:90 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:90 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:98 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:98 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:106 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:106 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: